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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=5; day=22; hr=12; min=43; sec=5; ms=375;]

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Application No: 10594258 Version No: 1.0

Input Set:**Output Set:**

Started: 2009-05-08 19:38:51.479
Finished: 2009-05-08 19:38:53.432
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 953 ms
Total Warnings: 12
Total Errors: 12
No. of SeqIDs Defined: 16
Actual SeqID Count: 16

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12) |

Input Set:

Output Set:

Started: 2009-05-08 19:38:51.479
Finished: 2009-05-08 19:38:53.432
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 953 ms
Total Warnings: 12
Total Errors: 12
No. of SeqIDs Defined: 16
Actual SeqID Count: 16

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |
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| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16) |

SEQUENCE LISTING

<110> Wageningen Centre for Food Sciences

<120> Novel mannose-specific adhesins and their use

<130> P212925EP

<140> 10594258

<141> 2009-05-08

<150> EP04075945.8

<151> 2004-03-23

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 1010

<212> PRT

<213> Lactobacillus plantarum

<400> 1

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20 25 30

Leu Gly Val Gly Thr Val Thr Met Thr Arg Ala Ala Ala Asp Ser
35 40 45

Glu Val Thr Asn Asp Ser Ala Ser Gln His Val Thr Ser Ile Ser Thr

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 50 | | | | | | 55 | | | | | | 60 | | | | |
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| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Asp | Asp | Lys | Ser | Val | Ser | Ala | Ser | Ile | Asn | Gln | Asp | Ala | Ser | Ala | Ser | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Val | Val | Asn | Lys | Ala | Val | Ser | Ala | Thr | Ser | Gln | Glu | Asn | Ser | Ser | Val | |
| | | | 100 | | | | | 105 | | | | | | 110 | | |
| Gln | Asn | Thr | Ser | Gln | Ala | Thr | Ser | Thr | Ser | Lys | Gln | Glu | Ser | Ser | Ser | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Thr | Lys | Asn | Thr | Ser | Gln | Thr | Thr | Ser | Thr | Ser | Asn | Gln | Glu | Ala | Asn | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Ser | Ala | Lys | Ser | Ile | Asn | Gln | Thr | Thr | Arg | Thr | Ser | Lys | Gln | Glu | Ser | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Ser | Ser | Thr | Lys | Asn | Thr | Ser | Gln | Thr | Thr | Ser | Thr | Ser | Asn | Gln | Glu | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Ala | Asn | Ser | Ala | Lys | Ser | Ile | Asn | Gln | Thr | Thr | Arg | Thr | Ser | Asn | Gln | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Glu | Ser | Ser | Ser | Ala | Lys | Asn | Thr | Ser | Gln | Thr | Thr | Ser | Thr | Ser | Ser | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Arg | Lys | Ile | Asn | Ser | Thr | Lys | Ser | Gln | Ala | Gln | Ser | Leu | Thr | Ile | Thr | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Thr | Thr | Gly | Lys | Ala | Val | Arg | Ala | Thr | Ser | Thr | Ser | Val | Lys | Lys | Tyr | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Ser | Thr | Lys | Thr | Lys | Val | Ser | Tyr | Ser | Thr | Leu | Leu | Gln | Gln | Leu | Arg | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Thr | Ser | Lys | Ala | Leu | Ile | Ser | Asp | Glu | Ala | Ala | Leu | Thr | His | Val | Asp | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Lys | Asp | Asn | Phe | Leu | Lys | Tyr | Phe | Ser | Leu | Asn | Gly | Ser | Ala | Thr | Tyr | |
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290 295 300

Val Gly Asn Phe Ser Leu Thr Ser Lys Ile Asp Met Asn Lys Ser Phe
305 310 315 320

Thr Leu Thr Gly Gln Val Asn Leu Gly Ser Asn Pro Asn Gly Ala Asp
325 330 335

Gly Ile Gly Phe Ala Phe His Ser Gly Asn Thr Thr Asp Val Gly Asn
340 345 350

Ala Gly Gly Asn Leu Gly Ile Gly Gly Leu Gln Asp Ala Ile Gly Phe
355 360 365

Lys Leu Asp Thr Trp Phe Asn Ser Tyr Gln Ala Pro Ser Ser Asp Lys
370 375 380

Asn Gly Ser Glu Ile Ser Ser Thr Asn Ser Asn Gly Phe Gly Trp Asn
385 390 395 400

Gly Asp Ser Ala Asn Ala Pro Tyr Gly Thr Phe Val Lys Thr Ser Asn
405 410 415

Gln Glu Ile Ser Thr Ala Asn Gly Ser Lys Val Gln Arg Trp Trp Ala
420 425 430

Gln Asp Thr Gly Glu Ser Gln Ala Leu Ser Lys Ala Asp Ile Asp Gly
435 440 445

Asn Phe His Asp Phe Val Val Asn Tyr Asp Gly Ala Thr Arg Thr Leu
450 455 460

Thr Val Ser Tyr Thr Gln Ala Ser Gly Lys Val Leu Thr Trp Lys Thr
465 470 475 480

Thr Val Asp Ser Ser Tyr Gln Ala Met Ala Met Val Val Ser Ala Ser
485 490 495

Thr Gly Ala Ala Lys Asn Leu Gln Gln Phe Lys Leu Thr Ser Phe Asp
500 505 510

Phe Gln Glu Ala Ala Thr Val Asn Val Lys Tyr Val Asp Thr Thr Gly
515 520 525

His Gln Leu Ala Gln Gly Thr Ala Asn Tyr Pro Asp Gly Ala Tyr Val
530 535 540

Asn Gly Arg Tyr Thr Thr Lys Gln Leu Ile Ile Pro Asn Tyr Arg Phe
545 550 555 560

Ile Lys Met Asp Asp Gly Ser Val Thr Gly Thr Lys Ser Leu Asp Ala
565 570 575

Asn Gly Thr Leu Ile Gln Ser Gly Asp Asn Gly Thr Val Ile Tyr Val
580 585 590

Tyr Val Pro Glu Tyr Met Ala Ile Val Lys Thr Val Asn Glu Thr Ile
595 600 605

Asn Tyr Val Asp Glu Asn Gly His Ala Leu Thr Thr Ser Tyr Thr Ala
610 615 620

Asn Pro Ile His Ile Leu Thr Val Thr Asn Pro Val Asp Gly Thr Thr
625 630 635 640

Thr Thr Tyr Tyr Ser Thr Ile Thr Thr Ser Ile Glu Leu Asp Ala Thr
645 650 655

Thr Gly Arg Pro Val Asp Ser Gly Trp Val Leu Gly Asn Ser Gln Asp
660 665 670

Phe Asp Ala Val Thr Asn Pro Gln Ile Lys Gly Tyr Thr Val Thr Ser
675 680 685

Thr Asp Ala Pro Asn Ser Asp Leu Gln His Val Ser Ala Gln Thr Val
690 695 700

Thr Gly Asp Ser Gly Asp Leu Glu Phe Thr Val Val Tyr Thr Lys Asn
705 710 715 720

Ala Pro Ile Val Thr Thr Glu Ser Lys Thr Val Asn Glu Thr Ile His
725 730 735

Tyr Val Tyr Thr Asp Gly Thr Thr Ala His Asp Asp Tyr Val Ala Gln
740 745 750

Pro Ile Thr Phe Thr Arg Thr Val Phe Thr Asp Ala Val Thr Gly Glu
755 760 765

Lys Thr Tyr Gly Gly Trp Ser Ala Ala Gln Gln Phe Ala Ala Val Asp
770 775 780

Ser Pro Ala Ile Lys Gly Tyr Thr Pro Asp Gln Ser Lys Ile Ser Thr
785 790 795 800

Gln Thr Val Thr Gly Asp Ser Ser Asp Leu Glu Phe Thr Ile Val Tyr
805 810 815

Thr Lys Asn Ala Pro Thr Val Thr Thr Glu Ser Lys Thr Val Asn Glu
820 825 830

Thr Ile His Tyr Val Tyr Thr Asp Gly Thr Ile Ala His Asp Asp Tyr
835 840 845

Val Ala Gln Pro Ile Thr Phe Thr Arg Thr Val Ser Thr Asp Ala Val
850 855 860

Thr Gly Glu Lys Thr Tyr Gly Gly Trp Ser Ala Ala Gln Gln Phe Ala
865 870 875 880

Ala Val Asp Ser Pro Ala Ile Lys Gly Tyr Thr Pro Asp Gln Ser Lys
885 890 895

Ile Ser Thr Gln Thr Val Thr Gly Asp Ser Ser Asp Leu Glu Phe Thr
900 905 910

Val Val Tyr Lys Ala Asp Ser Thr Ser Thr Lys Pro Val Lys Pro Glu
915 920 925

Gln Pro Thr Ile Pro Thr Thr Pro Thr Glu Pro Val Lys Pro Gly Gln
930 935 940

Leu Thr Thr Pro Ala Lys Pro Asp Gln Pro Met Thr Ser Asp Lys Ser
945 950 955 960

Val Gln Thr Ile Thr Ile Lys Phe Val Gly Gln Arg Leu Pro Gln Thr

965

970

975

Asn Glu Thr Asp Gln Gln His Met Thr Leu Ser Gly Leu Leu Leu Leu

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<213> Lactobacillus plantarum

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acacggggccg ccgcagcaga ttccgaagtg acgaacgatt cagcatctca acatgtgacg180

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gcggtcagcg caactagcca agaaaatagt agcgttcaaa atactagtca ggcaaccagt360

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| | |
|---|------|
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| gcttttcaca gtggcaatac aactgacgtg ggaaatgctg gtggtaattt aggtattggt | 1080 |
| ggattgcaag acgctatcgg gttcaagcta gacacatggg ttaatagcta ccaagcacca | 1140 |
| tcatcagata aaaatgggag tgaaatctca tcaacaaatt ctaatggctt tggttggaat | 1200 |
| ggtgactcag ccaacgcacc atatggcacc tttgtcaaga cgagtaacca agaaatttcg | 1260 |
| actgcgaatg gttctaaggt acagcgatgg tgggctcaag atacaggaga gtcgcaggcg | 1320 |
| ttaagtaaag cggatattga tggtaacttt catgattttg tagttaacta tgatggtgct | 1380 |
| acaagaacgt taaccgttag ttatacgcaa gctagtggta aagtattaac ttggaagacg | 1440 |
| actgttgaca gttcttatca agcaatggcc atggttgtca gtgcatcaac tggtgacgct | 1500 |
| aaaaatttac aacaatttaa gttgactagc ttcgattttc aagaagcagc gactgtgaat | 1560 |
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| atccaatcgg gtgacaatgg tactgttatc tatgtatatg tgccctgaata tatggctatt | 1800 |
| gtcaagacag ttaacgaaac tattaattat gttgatgaaa atggatcatgc gttgaccact | 1860 |
| agctacaccg ccaatcccat ccatatattg accgtgacga atccggtgga tggaacgacg | 1920 |
| acaacctact attcaacaat tacaacatcg atagaactag atgcgacaac tggtagacca | 1980 |
| gtcgattctg gatgggtatt gggtaatagt caagatttcg atgcagttac aaatccacaa | 2040 |
| atcaagggct atacagtaac aagtactgat gcgcctaatt cagatttgca gcatgtgtca | 2100 |
| gcgcagacgg ttactgggtga ttctgggtgac cttgaattta ccgtcgtgta caccaagaat | 2160 |
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| gcggccgtgg atagtccagc aattaagggc tacacaccag atcagagcaa aattagtacg | 2400 |
| cagaccgtta ctggcgattc cagtgcctt gaatttacca tcgtgtacac caagaatgct | 2460 |
| ccaaccgtga caacggaaag taaaacggtc aatgagacta ttcattatgt ttatacggat | 2520 |
| ggaactatag cccatgatga ttatgtggcc cagcccatca cgtttacacg gactgtatct | 2580 |
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<213> Lactobacillus plantarum

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Ile Lys Ser Trp Leu Val Ser Ser Tyr Ser Pro Thr Val Thr Ala Lys
35 40 45

Thr Val Lys Gln Asn Thr Lys Lys Lys Ser Asp Phe Asn Phe Ser Lys
50 55 60

Val Lys Ser Leu Asp Phe Gln Thr Val Ala Lys Ala Arg Met Asn Lys
65 70 75 80

Asn Ala Ile Asn Val Ile Gly Ser Ile Ala Ile Pro Ser Val Asp Leu
85 90 95

Tyr Leu Pro Ile Gly Asn Gly Val Ser Asn Glu Thr Leu Ala Leu Ala
100 105 110

Ala Gly Thr Met Lys Ala Asn Gln Lys Met Gly Gln Gly Asn Tyr Ala
115 120 125

Leu Ala Gly His His Met Ile Lys His Gly Ala Leu Phe Ser Pro Leu
130 135 140

Tyr Tyr Lys Ser Lys Val Gly Gln Met Ile Tyr Val Ser Asp Ala Lys
145 150 155 160

Lys Ile Tyr Ala Tyr Lys Thr Ser Gln Arg Thr Phe Ile Lys Ala Thr
165 170 175

Asp Val Gln Val Ile Asp Asp Val Pro Gly Gln Lys Leu Ile Thr Leu
180 185 190

Ile Thr Cys Asp Lys Thr Gly Ala Gly Arg Leu Met Ile Arg Gly Lys
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tactcgccga ccgttacggc taagacgggt aagcagaata cgaagaagaa gagcgatttt 180
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attgatgatg ttcttggtca gaagctgatt accctaatta cctgtgataa gaccggggcg 600
ggtcgcttaa tgattcgcgg taagtacgaa cagcaatggt cgtttaagtc ggcgccaact 660
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